



PATENT
0020-4546P

IN THE U.S. PATENT AND TRADEMARK OFFICE

Applicant: KIMURA, Toru et al. Conf.: 1992
Appl. No.: 09/284,180 Group: 1633
Filed: June 9, 1999 Examiner: S. Chen
For: NOVEL SEMAPHORIN GENE: SEMAPHORIN W

HAWKINS DECLARATION

Assistant Commissioner for Patents February 25, 2003
Washington, DC 20231

Sir:

The specification of the above-referenced application is amended to include material incorporated by reference. Specifically, the specification is amended to include GenBank Accession No: T09073 in the substitute Sequence Listing as SEQ ID NO: 15. The nucleotide sequence of GenBank Accession No: T09073 was created on May 25, 1993 and last updated on August 3, 1993, and disclosed in the specification as filed on June 9, 1999, for example on page 49, lines 1-5 and 16-22. Therefore, the amendatory material (i.e., SEQ ID NO:15) consists of the same material (i.e., GenBank Accession No: T09073) incorporated by reference in the referencing application at the time of filing. No new matter is added to the application.

If necessary, the Commissioner is hereby authorized in this,

Application No.: 09/284,180

concurrent, and future replies, to charge payment or credit any overpayment to Deposit Account No. 02-2448 for any additional fees required under 37 C.F.R. §§ 1.16 or 1.17; particularly, extension of time fees.

Respectfully submitted,
BIRCH, STEWART, KOLASCH & BIRCH, LLP

By

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0020-4546P

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Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.4 [Aug-26-2002]

Match: 1 Mismatch: -2 gap open: 5 gap extension: 2

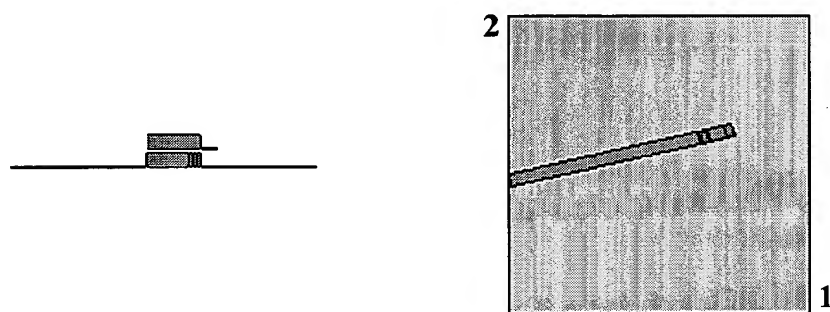
x_dropoff: expect: wordsize: Filter ☒

Sequence gi yg78f12.r1 Soares infant brain 1NIB Homo sapiens cDNA
1 816289 clone IMAGE:39491 5' similar to SP:A49069 A49069
COLLAPSIN - .:

Length 517 (1 .. 517)

Sequence 1cl|seq_2

Length 2331 (1 .. 2331)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE:If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 483 bits (251), Expect = e-133
Identities = 344/385 (89%), Gaps = 3/385 (0%)
Strand = Plus / Plus



```
Query: 1      gaccacaagacattcggacagtgtgaatgggcccttcagagaactaaaacatgactgca 60
            ||||| ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 1052  gaccccaagacatccgggcagtgtgaatgggccctttagagagctaaaacatgactgca 1111
```

Query: 61 acagaggactgcctgtcgtggacaatgatgtgccccagcccagacctggagagtgcac 120
||||| ||||||| ||||| || ||||||| ||||||| ||||||| ||||||| |||||
Sbjct: 1112 acaggggactgcctgtcatggacaacgaggtgccccagcccagacctggagagtgcac 1171

Query: 121 ccaacaacatgaagctccggcactttggctcatctctctccctgcctgaccgcgtactca 180
 |||
 Sbjct: 1172 ccaacaacatgaagctccagcagtttgatcctcactctccctgccagaccgcgtgctca 1231

Query: 181 ccttcacccgggancacccactcatggacaggccagntttccagctgatggccacccc 240

Sbjct: 1232 cctttatcagaqaccacctctcatggacagqcccgtgttcccggctgacggccgcccc 1291

Query: 241 tgntggtcactacagatacagnc¹tatctcagagtcgtggcccacaggg²tgaccagcctct 300

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

Sbjct: 1292 tgctggtcactacagatacagcctatctcagagtcgtggccacaggggtgaccagcctct 1351

1361

Query: 301 cagggaaagagtatgatgtgctctacctgggggacagaggatgggacaacttcaccgagc 360

[illegible]

Sbjct: 1352 cagggaaagaatatgacgtgctctacct-ggggacagaggat-ggacacctccaccgggc 1409

Query: 361 agtgcggattcggagctcagttcag 385

[illegible]

Subject: 1410 tqtgcgcatt-ggagctcagctcag 1433

```
CPU time:      0.06 user secs.      0.07 sys. secs      0.13 total secs.
```

Lambda	K	H
1.33	0.621	1.12

Gapped			
Lambda	K	H	
1.33	0.621	1.12	

```

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 3
Number of Sequences: 0
Number of extensions: 3
Number of successful extensions: 2
Number of sequences better than 10.0: 1
length of query: 517
length of database: 7,880,065,999
effective HSP length: 24
effective length of query: 493
effective length of database: 7,880,065,975
effective search space: 3884872525675
effective search space used: 3884872525675
T: 0
A: 0
X1: 6 (11.5 bits)
X2: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 20 (39.1 bits)

```



Blast 2 Sequences results

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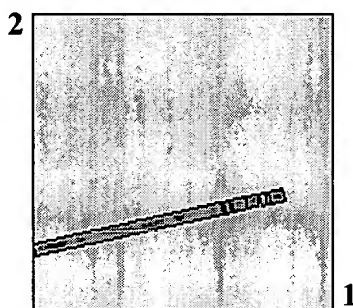
BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.4 [Aug-26-2002]

 Match: Mismatch: gap open: gap extension:

 x_dropoff: expect: wordsize: Filter ☒ **Align**

Sequence gi yg78f12.r1 Soares infant brain 1NIB Homo sapiens cDNA
 1 816289 clone IMAGE:39491 5' similar to SP:A49069 A49069 Length 517 (1 .. 517)
 COLLAPSIN - ;

Sequence lcl|seq_2 Length 2315 (1 .. 2315)
 2



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 675 bits (351), Expect = 0.0
 Identities = 413/432 (95%), Gaps = 7/432 (1%)
 Strand = Plus / Plus

438
 ↓

```

Query: 1  gaccacaagacattcggacagtgcgtgaatgggcccttcagagaactaaaacatgactgca 60
          |||
Sbjct: 488 gaccacaagacattcggacagtgcgtgaatgggcccttcagagaactaaaacatgactgca 547

Query: 61  acagaggactgcctgtcgtggacaatgatgtgccccagcccagacctggagagtgcacatca 120
          |||
Sbjct: 548 acagaggactgcctgtcgtggacaatgatgtgccccagcccagacctggagagtgcacatca 607

Query: 121 ccaacaacatgaagctccggcactttggctcatctctccctgcctgaccgcgtactca 180
          |||
Sbjct: 608 ccaacaacatgaagctccggcactttggctcatctctccctgcctgaccgcgtactca 667

Query: 181 ccttcatccgggancaccactcatggacaggccagtnnttccagctgatggccaccccc 240
          |||
  
```

Sbjct: 668 ccttcatccgggaccacccactcatggacaggccagtggtttccagctgatggccaccccc 727

Query: 241 tgntgggtcactacagatacagnctatctcagagtcgtggcccacagggtgaccagcctct 300
|| |||||

Sbjct: 728 tgctgggtcactacagatacagcctatctcagagtcgtggcccacagggtgaccagcctct 787

Query: 301 cagggaaagagtatgatgtgctctacctgggggacagaggatgggacaacttcaccgagc 360
|| |||||

Sbjct: 788 cagggaaagagtatgatgtgctctacct-ggggacagaggat-ggacacctccaccgagc 845

Query: 361 agtgcggattcggagctcagttcagcgtttctttgaagatcttgggcttatttnccagag 420
|| |||||

Sbjct: 846 agtgcgga-tcggagctcagctcagcgtt--cttgaagatc-tggcctta-ttcccagag 900

Query: 421 tcacagncagtt 432

|||||

Sbjct: 901 ccacagccagtt 912

CPU time: 0.08 user secs. 0.02 sys. secs 0.10 total secs.

Lambda	K	H
1.33	0.621	1.12

Gapped

Lambda	K	H
1.33	0.621	1.12

Matrix: blastn matrix:1 -2

Gap Penalties: Existence: 5, Extension: 2

Number of Hits to DB: 4

Number of Sequences: 0

Number of extensions: 4

Number of successful extensions: 4

Number of sequences better than 10.0: 1

length of query: 517

length of database: 7,880,065,999

effective HSP length: 24

effective length of query: 493

effective length of database: 7,880,065,975

effective search space: 3884872525675

effective search space used: 3884872525675

T: 0

A: 0

X1: 6 (11.5 bits)

X2: 26 (50.0 bits)

S1: 12 (23.8 bits)


S2: 20 (39.1 bits)



Blast 2 Sequences results

[PubMed](#)[Entrez](#)[BLAST](#)[OMIM](#)[Taxonomy](#)[Structure](#)

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.4 [Aug-26-2002]

Match: Mismatch: gap open: gap extension: x_dropoff: expect: wordsize: Filter ☒ 

Sequence	gi	yg78f12.r1 Soares infant brain 1NIB Homo sapiens cDNA clone	Length	517
1	<u>816289</u>	IMAGE:39491 5' similar to SP:A49069 A49069 COLLAPSIN - ;		

Sequence	lcl seq_2	Length	333
2			

No significant similarity was found

Seq ID NO: 10